

Amendments to the Specification:

Please amend the specification as follows:

Please replace the bottom paragraph number on page 16, with the following rewritten paragraph:

[0048] "Sequence identity" is defined herein with reference the Blast 2 algorithm, which is available at the NCBI (~~http://www.ncbi.nlm.nih.gov/BLAST~~), (www.ncbi.nlm.nih.gov/BLAST), using default parameters. References pertaining to this algorithm include: those found at http://www.ncbi.nlm.nih.gov/BLAST/blast_references.html; www.ncbi.nlm.nih.gov/BLAST/blast_references.html; Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215: 403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3: 266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266: 131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25: 3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7: 649-656. Accordingly, the prolactin peptide sequences from different species, which include those listed in Table 1, can be aligned, using standard computer programs like BLAST, to inform further variation in prolactin-derived receptor-antagonizing domains that preserve their essential function.